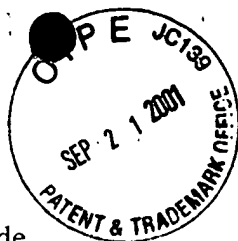


#4



SEQUENCE LISTING

<110> Miyake, Katsuhide
Watanabe, Masaki
Iijima, Shinji

<120> Beta 1,3-galactosyltransferase and DNA encoding the same

<130> 766.53

<140> US 09/900,038

<141> 2001-07-09

<150> JP 2001-392

<151> 2001-01-05

<160> 8

<170> PatentIn Ver. 2.0

<210> 1

<211> 313

<212> PRT

<213> Streptococcus agalactiae Type Ib

<400> 1

Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn Tyr
1 5 10 15

Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp Phe
20 25 30

Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys Gln
35 40 45

Phe Leu Thr Glu Tyr Ser Val Val Asp Asn Arg Ile Lys Ile Leu Leu
50 55 60

Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val Lys
65 70 75 80

Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile Ser
85 90 95

Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn Ser
100 105 110

Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly Asn
115 120 125

Leu Val Tyr Lys Gln Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn Asp
130 135 140

Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr Trp
145 150 155 160

Cys Val Lys Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp Leu
165 170 175

Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala Asp
180 185 190

Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu Asn
195 200 205

Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr Ser
210 215 220

Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile Thr
225 230 235 240

Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr Thr
245 250 255

Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser Ile
260 265 270

Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser Pro
275 280 285

Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu Lys
290 295 300

Leu Phe Gly Gly Glu Lys Gln Ser Asp
305 310

<210> 2

<211> 939

<212> DNA

<213> Streptococcus agalactiae Type Ib

<400> 2

atg aat tat agt atc att atg tcg gta tat aat gag cct tta aat tat 48

Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn Tyr
1 5 10 15

gtg aga gat tca gta gaa tct ata tta aat caa acg ctt act gat ttt 96
Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp Phe
20 25 30

gag ttc ata att gtc att gat aat cca agt aga ggt gat tta aag caa 144
Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys Gln
35 40 45

ttc tta aca gaa tat tca gtt gta gat aat aga ata aaa atc ttg ctt 192
Phe Leu Thr Glu Tyr Ser Val Val Asp Asn Arg Ile Lys Ile Leu Leu
50 55 60

aat gaa gaa aat att ggt tta gca tca agt ttg aac aaa gcg gtg aaa 240
Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val Lys
65 70 75 80

att tct aag gga gaa tat att ttt aga atg gat gct gat gat att tca 288
Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile Ser
85 90 95

tat cca agt aga ttt gat aag caa att cgt ttt atg gag gaa aat tca 336
Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn Ser
100 105 110

ttg gat ttc tca gca act cta ata gaa ttg ata gac caa aaa gga aat 384
Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly Asn
115 120 125

tta gta tat aaa caa cga gaa agt aat aaa ata tac tta act aat gat 432
Leu Val Tyr Lys Lys Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn Asp
130 135 140

ata cgg aag atg tta ttg aat aga tct ata ctt gcc cac cca acg tgg 480
Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr Trp
145 150 155 160

tgc gta aaa aag aaa gtt ttc gat aag tta atg gga tat aga gat tta 528
Cys Val Lys Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp Leu
165 170 175

gta cct gtt gaa gat tat gat ttt gca ata aga gga gct ctg gct gat 576
Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala Asp

180	185	190	
ttc aaa atc ggc tta ctc aat aaa gta ctt tta cag tat aga tta aac 624			
Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu Asn			
195	200	205	
gag aat gga ata tca caa acc aat aag ttt aag caa tat att tac tca 672			
Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr Ser			
210	215	220	
gct att tta caa gat ttt tat aaa gaa aaa tct tat att gat atc aca 720			
Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile Thr			
225	230	235	240
aaa att act aat tac ttt caa gag tat gtg ata aag aaa cgc tat act 768			
Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr Thr			
245	250	255	
cag caa gag ctc tct aaa tat ttt gag cta aaa tct acc cct agt att 816			
Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser Ile			
260	265	270	
act att aga aaa cta tat att tgt tta tat tta tac ttt aag tct ccc 864			
Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser Pro			
275	280	285	
ttg gtt agg agg tta tta ata aat gat att aat att tta gta ctg aaa 912			
Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu Lys			
290	295	300	
ttg ttt gga gga gag aaa caa agt gac 939			
Leu Phe Gly Gly Glu Lys Gln Ser Asp			
305	310		

<210> 3
 <211> 6865
 <212> DNA
 <213> Streptococcus agalactiae type Ib

<220>
 <221> CDS
 <222> (617)..(1789)

<220>

<221> CDS
<222> (1816)..(2262)

<220>
<221> CDS
<222> (2265)..(2744)

<220>
<221> CDS
<222> (2843)..(3979)

<220>
<221> CDS
<222> (3982)..(4953)

<220>
<221> CDS
<222> (5009)..(5947)

<400> 3
agatcttgga gatattatct gtgaaaccaa tgttcctaga ctgatggtcg ttccttcagg 60
gaaagtacca ccaaatacaa cagcattact tcagaacgct tattttaata agatgattga 120
agctattaaa aatatatttg attatattat catcgatact ccacctattg gtttagttgt 180
tgatgccgca ataatcgcta atgcttgcca tggttttatt ttagtaaccc aagcaggtag 240
aataaaacgt aattatgttg aaaaagcaaa agaacagatg gaacaaagtg gttcaaagtt 300
cttaggtatt attcttaata aagttaatga atctgttgct acttacggcg attatggaaa 360
ttacggaaaa agggatagaa aaaggaagta aggggctctt gtattgaaag aaaaagaaaa 420
tatacaaaag attattatag cgatgattca aaccgttggt gtttattttt ctgcaagttt 480
gacattaaca ttaattactc ccaactttaa aagcaataaa gatttattgt ttgttctatt 540
gatacattat attgtctttt atctttctga tttttacaga gacttttgga gtcgtggcta 600
tcttgaagag tttaaa atg gta ttg aaa tac agc ttt tac tat att ttc ata 652
Met Val Leu Lys Tyr Ser Phe Tyr Tyr Ile Phe Ile
1 5 10
tca agt tca tta ttt ttt att tct aaa aac tct ttt aca acg aca cga 700

Ser Ser Ser Leu Phe Phe Ile Ser Lys Asn Ser Phe Thr Thr Thr Arg
15 20 25

ctt tcc ttt ttt act ttt att gct atg aat tcg att tta tta tat cta 748
Leu Ser Phe Phe Thr Phe Ile Ala Met Asn Ser Ile Leu Leu Tyr Leu
30 35 40

ttg aat tca ttt tta aaa tat tat cga aaa tat tct tac gct aag ttt 796
Leu Asn Ser Phe Leu Lys Tyr Tyr Arg Lys Tyr Ser Tyr Ala Lys Phe
45 50 55 60

tca cga gat acc aaa gtt gtt ttg ata acg aat aag gat tct tta tca 844
Ser Arg Asp Thr Lys Val Val Leu Ile Thr Asn Lys Asp Ser Leu Ser
65 70 75

aaa atg acc ttt agg aat aaa tac gac cat aat tat atc gct gtc tgt 892
Lys Met Thr Phe Arg Asn Lys Tyr Asp His Asn Tyr Ile Ala Val Cys
80 85 90

atc ttg gat tcc tct gaa aag gat tgt tat gat ttg aaa cat aac tcg 940
Ile Leu Asp Ser Ser Glu Lys Asp Cys Tyr Asp Leu Lys His Asn Ser
95 100 105

tta agg ata ata aac aaa gat gct ctt act tca gag tta acc tgc tta 988
Leu Arg Ile Ile Asn Lys Asp Ala Leu Thr Ser Glu Leu Thr Cys Leu
110 115 120

act gtt gat caa gct ttt att aac ata ccc att gaa tta ttt ggt aaa 1036
Thr Val Asp Gln Ala Phe Ile Asn Ile Pro Ile Glu Leu Phe Gly Lys
125 130 135 140

tac caa ata caa gat att att aat gac att gaa gca atg gga gtg att 1084
Tyr Gln Ile Gln Asp Ile Ile Asn Asp Ile Glu Ala Met Gly Val Ile
145 150 155

gtc aat gtt aat gta gag gca ctt agc ttt gat aat ata gga gaa aag 1132
Val Asn Val Asn Val Glu Ala Leu Ser Phe Asp Asn Ile Gly Glu Lys
160 165 170

cga atc caa act ttt gaa gga tat agt gtt att aca tat tct atg aaa 1180
Arg Ile Gln Thr Phe Glu Gly Tyr Ser Val Ile Thr Tyr Ser Met Lys
175 180 185

ttc tat aaa tat agt cac ctt ata gca aaa cga ttt ttg gat atc atg 1228
Phe Tyr Lys Tyr Ser His Leu Ile Ala Lys Arg Phe Leu Asp Ile Met

190	195	200	
ggt gct att ata ggt ttg ctc ata tgt ggc att gtg gca att ttt cta 1276			
Gly Ala Ile Ile Gly Leu Leu Ile Cys Gly Ile Val Ala Ile Phe Leu			
205	210	215	220
ggt ccg caa atc aga aaa gat ggt gga ccg gct atc ttt tct caa aat 1324			
Val Pro Gln Ile Arg Lys Asp Gly Gly Pro Ala Ile Phe Ser Gln Asn			
225	230	235	
aga gta ggt cgt aat ggt agg att ttt aga ttc tat aaa ttc aga tca 1372			
Arg Val Gly Arg Asn Gly Arg Ile Phe Arg Phe Tyr Lys Phe Arg Ser			
240	245	250	
atg cga gta gat gca gaa caa att aag aaa gat tta tta gtt cac aat 1420			
Met Arg Val Asp Ala Glu Gln Ile Lys Lys Asp Leu Leu Val His Asn			
255	260	265	
caa atg acg ggg cta atg ttt aag tta gac gat gat cct aga att act 1468			
Gln Met Thr Gly Leu Met Phe Lys Leu Asp Asp Asp Pro Arg Ile Thr			
270	275	280	
aaa ata gga aaa ttt att cga aaa aca agc ata gat gag ttg cct caa 1516			
Lys Ile Gly Lys Phe Ile Arg Lys Thr Ser Ile Asp Glu Leu Pro Gln			
285	290	295	300
ttc tat aat gtt tta aaa ggt gat atg agt tta gta gga aca cgc cct 1564			
Phe Tyr Asn Val Leu Lys Gly Asp Met Ser Leu Val Gly Thr Arg Pro			
305	310	315	
ccc aca gtt gat gaa tat gaa aag tat aat tca acg cag aag cga cgc 1612			
Pro Thr Val Asp Glu Tyr Gly Lys Tyr Asn Ser Thr Gln Lys Arg Arg			
320	325	330	
ctt agt ttt aag cca gga atc act ggt ttg tgg caa ata tct ggt aga 1660			
Leu Ser Phe Lys Pro Gly Ile Thr Gly Leu Trp Gln Ile Ser Gly Arg			
335	340	345	
aat aat att act gat ttt gat gaa atc gta aag tta gat gtt caa tat 1708			
Asn Asn Ile Thr Asp Phe Asp Glu Ile Val Lys Leu Asp Val Gln Tyr			
350	355	360	
atc aat gaa tgg tct att tgg tca gat att aag att att ctc cta acg 1756			
Ile Asn Glu Trp Ser Ile Trp Ser Asp Ile Lys Ile Ile Leu Leu Thr			
365	370	375	380

cta aag gta gtt tta ctc ggg aca gga gct aag taaaggttaag gtttgaaagg 1809
Leu Lys Val Val Leu Leu Gly Thr Gly Ala Lys
385 390

aatata atg aaa att tgt ctg gtt ggt tca agt ggt ggt cac cta gca 1857
Met Lys Ile Cys Leu Val Gly Ser Ser Gly Gly His Leu Ala
395 400 405

cac ttg aac ctt ttg aaa ccc att tgg gaa aaa gaa gat agg ttt tgg 1905
His Leu Asn Leu Leu Lys Pro Ile Trp Glu Lys Glu Asp Arg Phe Trp
410 415 420

gta act ttt gat aaa gaa gat gct agg agt att cta aga gaa gag att 1953
Val Thr Phe Asp Lys Glu Asp Ala Arg Ser Ile Leu Arg Glu Glu Ile
425 430 435

gta tat cat tgc ttc ttt cca aca aac cgt aat gtc aaa aac ttg gta 2001
Val Tyr His Cys Phe Phe Pro Thr Asn Arg Asn Val Lys Asn Leu Val
440 445 450

aaa aat act att cta gct ttt aag gtc ctt aga aaa gaa aga cca gat 2049
Lys Asn Thr Ile Leu Ala Phe Lys Val Leu Arg Lys Glu Arg Pro Asp
455 460 465

gtt atc ata tca tct ggt gcc gct gta gca gta cca ttc ttt tat att 2097
Val Ile Ile Ser Ser Gly Ala Ala Val Ala Val Pro Phe Phe Tyr Ile
470 475 480 485

ggg aag tta ttt ggc tgt aag acc gtt tat ata gag gtt ttc gac agg 2145
Gly Lys Leu Phe Gly Cys Lys Thr Val Tyr Ile Glu Val Phe Asp Arg
490 495 500

ata gat aaa cca act ttg aca gga aaa tta gtg tat cct gta aca gat 2193
Ile Asp Lys Pro Thr Leu Thr Gly Lys Leu Val Tyr Pro Val Thr Asp
505 510 515

aaa ttt att gtt cag tgg gaa gaa atg aaa aaa gtt tat cct aag gca 2241
Lys Phe Ile Val Gln Trp Glu Glu Met Lys Lys Val Tyr Pro Lys Ala
520 525 530

att aat tta gga gga att ttt ta atg att ttt gtc aca gta ggg aca 2288
Ile Asn Leu Gly Gly Ile Phe Met Ile Phe Val Thr Val Gly Thr
535 540 545

cat gaa cag cag ttc aac cgt ctt att aaa gaa gtt gat aga tta aaa 2336

His Glu Gln Gln Phe Asn Arg Leu Ile Lys Glu Val Asp Arg Leu Lys
550 555 560

ggg aca ggt gct att gat caa gaa gtg ttc att caa acg ggt tac tca 2384
Gly Thr Gly Ala Ile Asp Gln Glu Val Phe Ile Gln Thr Gly Tyr Ser
565 570 575 580

gac ttt gaa cct cag aat tgt cag tgg tca aaa ttt ctc tca tat gat 2432
Asp Phe Glu Pro Gln Asn Cys Gln Trp Ser Lys Phe Leu Ser Tyr Asp
585 590 595

gat atg aac tct tac atg aaa gaa gct gag att gtt atc aca cac ggc 2480
Asp Met Asn Ser Tyr Met Lys Glu Ala Glu Ile Val Ile Thr His Gly
600 605 610

ggg cca gca acg ttt atg aat gca gtt tct aaa ggg aaa aaa act att 2528
Gly Pro Ala Thr Phe Met Asn Ala Val Ser Lys Gly Lys Lys Thr Ile
615 620 625

gtg gtt cct aga caa gaa cag ttt gga gag cat gtg aat aat cat cag 2576
Val Val Pro Arg Gln Glu Gln Phe Gly Glu His Val Asn Asn His Gln
630 635 640

gtg gat ttt ttg aaa gag tta ttc ttg aaa tat gag tta gat tat att 2624
Val Asp Phe Leu Lys Glu Leu Phe Leu Lys Tyr Glu Leu Asp Tyr Ile
645 650 655 660

ttg aat atc agt gaa tta gag aat att att aag gaa aaa aat ata tct 2672
Leu Asn Ile Ser Glu Leu Glu Asn Ile Ile Lys Glu Lys Asn Ile Ser
665 670 675

act agt aaa gta ata tca caa aac aat gat ttt tgt tcc tct ttc aaa 2720
Thr Ser Lys Val Ile Ser Gln Asn Asn Asp Phe Cys Ser Ser Phe Lys
680 685 690

aat gaa ctt tct aaa cta ttt gaa taaatatatt ttgttgaga aaaaaattga 2774
Asn Glu Leu Ser Lys Leu Phe Glu
695 700

aattaactat caatccaaag tatttgtaa taggaggaat ttctgctta accctatttt 2834

caaagcca atg caa ctt ttg tta ctt tta gca tta ata gtt tta ctt att 2884
Met Gln Leu Leu Leu Leu Leu Ala Leu Ile Val Leu Leu Ile
705 710

tgt agt agt tat aat gaa aaa atg aaa ttt tta aat atg gct gaa att 2932
Cys Ser Ser Tyr Asn Glu Lys Met Lys Phe Leu Asn Met Ala Glu Ile
715 720 725 730

ttt ttc att gta ttt tat atg gtt tat tta gta tca ata gta tta aat 2980
Phe Phe Ile Val Phe Tyr Met Val Tyr Leu Val Ser Ile Val Leu Asn
735 740 745

tcg tta ttt aga agt cca gaa ttt cat aga gtc att gct gca ttc aat 3028
Ser Leu Phe Arg Ser Pro Glu Phe His Arg Val Ile Ala Ala Phe Asn
750 755 760

tca ctg gca gta ggg gtt gtg tcc tta tta ttt tac cat tac tat aag 3076
Ser Leu Ala Val Gly Val Val Ser Leu Leu Phe Tyr His Tyr Tyr Lys
765 770 775

aat act aat att gaa tta aca aaa ttg cta aaa tca ttt ttg ttt aat 3124
Asn Thr Asn Ile Glu Leu Thr Lys Leu Leu Lys Ser Phe Leu Phe Asn
780 785 790

gca att att ttg ttt tgt tta gga ttt cta tat tat tat gcc ata tat 3172
Ala Ile Ile Leu Phe Cys Leu Gly Phe Leu Tyr Tyr Tyr Ala Ile Tyr
795 800 805 810

ttt gat gta gag aat gta agt ctt ttt gga aga aat tta att gga tca 3220
Phe Asp Val Glu Asn Val Ser Leu Phe Gly Arg Asn Leu Ile Gly Ser
815 820 825

gat tgg ata aat ggg atg cat acg cag aga gca atg gct ttc ttt gaa 3268
Asp Trp Ile Asn Gly Met His Thr Gln Arg Ala Met Ala Phe Phe Glu
830 835 840

tat tca aat ctt ata ata ccc tta act atc ata act aat ata tat ata 3316
Tyr Ser Asn Leu Ile Ile Pro Leu Thr Ile Ile Thr Asn Ile Tyr Ile
845 850 855

tat ata tat att aag caa aga tat agc tca ggg atg atg ata ctc ggt 3364
Tyr Ile Tyr Ile Lys Gln Arg Tyr Ser Ser Gly Met Met Ile Leu Gly
860 865 870

gct ctt ctc tcc act att ata cta ccc atc ggg tct gga tct aga gct 3412
Ala Leu Leu Ser Thr Ile Ile Leu Pro Ile Gly Ser Gly Ser Arg Ala
875 880 885 890

ggc att ata gtt gtg cta cta cag gtt ata att tta ttg ttg aat aca 3460

Gly Ile Ile Val Val Leu Leu Gln Val Ile Ile Leu Leu Leu Asn Thr
895 900 905

att gta ata aaa aga caa acg ata aga ttt ttc ctg tat tta gtt ccg 3508
Ile Val Ile Lys Arg Gln Thr Ile Arg Phe Phe Leu Tyr Leu Val Pro
910 915 920

ata cta ata tta cta tta gtg ata tta cgt ttt gat aat ttg gtg agc 3556
Ile Leu Ile Leu Leu Leu Val Ile Leu Arg Phe Asp Asn Leu Val Ser
925 930 935

ata tat aat aga ata atc aat ttg cgg tcg gga agt agt gaa tct aga 3604
Ile Tyr Asn Arg Ile Ile Asn Leu Arg Ser Gly Ser Ser Glu Ser Arg
940 945 950

ttt tct ttg tac aag gat acc gta cac tca gta att act gac tca cta 3652
Phe Ser Leu Tyr Lys Asp Thr Val His Ser Val Ile Thr Asp Ser Leu
955 960 965 970

ttt ctg gga aaa ggt gta aaa gaa ttg tgg tta aat agt gat tta cca 3700
Phe Leu Gly Lys Gly Val Lys Glu Leu Trp Leu Asn Ser Asp Leu Pro
975 980 985

cta gga tcg cat tcg acc tac ata ggt tat ttc tat aaa act ggc cta 3748
Leu Gly Ser His Ser Thr Tyr Ile Gly Tyr Phe Tyr Lys Thr Gly Leu
990 995 1000

ttt gga cta ata aat gtg att tta ggt ttg ttt cta att ctt att agc 3796
Phe Gly Leu Ile Asn Val Ile Leu Gly Leu Phe Leu Ile Leu Ile Ser
1005 1010 1015

att atc aag gaa gct aaa aag tca gat ttc tat tat gag ata gta ggg 3844
Ile Ile Lys Glu Ala Lys Lys Ser Asp Phe Tyr Tyr Glu Ile Val Gly
1020 1025 1030

tct gtc ata ctc cta ttt tca ttt ttt gca ctt gaa gat att gat ggc 3892
Ser Val Ile Leu Leu Phe Ser Phe Phe Ala Leu Glu Asp Ile Asp Gly
1035 1040 1045 1050

gcc aat tgg ctc att att ttt gtc ttt aca gtg ttg gga att tta gaa 3940
Ala Asn Trp Leu Ile Ile Phe Val Phe Thr Val Leu Gly Ile Leu Glu
1055 1060 1065

aat aag gat ttc tat agt caa ctt aaa agg tgg gaa agt ta atg gaa 3987
Asn Lys Asp Phe Tyr Ser Gln Leu Lys Arg Trp Glu Ser Met Glu

1070	1075	1080	
aaa caa ata ctt gtt tct atc gtt ata cct ata tac aac tcg gaa gca 4035			
Lys Gln Ile Leu Val Ser Ile Val Ile Pro Ile Tyr Asn Ser Glu Ala			
1085	1090	1095	
tat ctt aaa gaa tgc gtg caa tcc gtc cta caa cag act cat tca ttg 4083			
Tyr Leu Lys Glu Cys Val Gln Ser Val Leu Gln Gln Thr His Ser Leu			
1100	1105	1110	
ata gaa gtt ata ctg att aat gat gga tcc act gat aat agt gga gaa 4131			
Ile Glu Val Ile Leu Ile Asn Asp Gly Ser Thr Asp Asn Ser Gly Glu			
1115	1120	1125	
att tgt gat aat tta tct caa aaa gac gat cgc ata ctt gta ttt cat 4179			
Ile Cys Asp Asn Leu Ser Gln Lys Asp Asp Arg Ile Leu Val Phe His			
1130	1135	1140	1145
aaa aaa aat gga ggg gta tct tcg gca agg aac cta ggt ctt gat aaa 4227			
Lys Lys Asn Gly Gly Val Ser Ser Ala Arg Asn Leu Gly Leu Asp Lys			
1150	1155	1160	
tcc aca ggc gaa ttc ata acg ttt gta gat agt gat gat ttt gta gca 4275			
Ser Thr Gly Glu Phe Ile Thr Phe Val Asp Ser Asp Asp Phe Val Ala			
1165	1170	1175	
ccg aat ata att gaa ata atg tta aaa aat tta atc act gag gat gct 4323			
Pro Asn Ile Ile Glu Ile Met Leu Lys Asn Leu Ile Thr Glu Asp Ala			
1180	1185	1190	
gat ata gca gaa gta gat ttt gat att tcg aat gag aga gat tat aga 4371			
Asp Ile Ala Glu Val Asp Phe Asp Ile Ser Asn Glu Arg Asp Tyr Arg			
1195	1200	1205	
aag aaa aaa aga cga aac ttt tat aag gtc ttt aaa aac aat aat tct 4419			
Lys Lys Lys Arg Arg Asn Phe Tyr Lys Val Phe Lys Asn Asn Asn Ser			
1210	1215	1220	1225
tta aaa gaa ttt tta tca ggt aat aga gtg gaa aat att gtt tgt aca 4467			
Leu Lys Glu Phe Leu Ser Gly Asn Arg Val Glu Asn Ile Val Cys Thr			
1230	1235	1240	
aaa tta tat aaa aaa agt ata att ggt aac ttg agg ttt gat gag aat 4515			
Lys Leu Tyr Lys Lys Ser Ile Ile Gly Asn Leu Arg Phe Asp Glu Asn			
1245	1250	1255	

tta aaa att ggt gag gat tta ctt ttt aat tgt aaa att tta tgt caa 4563
Leu Lys Ile Gly Glu Asp Leu Leu Phe Asn Cys Lys Ile Leu Cys Gln
1260 1265 1270

gag cac tgc ata gtc gta gat acg act tct tcc ttg tac acc tat cgc 4611
Glu His Cys Ile Val Val Asp Thr Thr Ser Ser Leu Tyr Thr Tyr Arg
1275 1280 1285

atc gta aag act tct gca atg aat cag gag ttc aac gaa aat tca tta 4659
Ile Val Lys Thr Ser Ala Met Asn Gln Glu Phe Asn Glu Asn Ser Leu
1290 1295 1300 1305

gat ttt ata aca att ttt aat gaa ata agc agt att gtt cct gca aaa 4707
Asp Phe Ile Thr Ile Phe Asn Glu Ile Ser Ser Ile Val Pro Ala Lys
1310 1315 1320

tta gct aat tat gtt gaa gcg aaa ttt tta aga gaa aag gta aag tgt 4755
Leu Ala Asn Tyr Val Glu Ala Lys Phe Leu Arg Glu Lys Val Lys Cys
1325 1330 1335

ctc cga aaa atg ttt gaa tta ggt agt aat att gac agt aaa atc aaa 4803
Leu Arg Lys Met Phe Glu Leu Gly Ser Asn Ile Asp Ser Lys Ile Lys
1340 1345 1350

tta caa cga gag att ttt ttc aaa gat gtt aaa tta tac cct ttc tat 4851
Leu Gln Arg Glu Ile Phe Phe Lys Asp Val Lys Leu Tyr Pro Phe Tyr
1355 1360 1365

aaa gcg gtt aag tac tta tca tta aag gga tta ttg agt att tac tta 4899
Lys Ala Val Lys Tyr Leu Ser Leu Lys Gly Leu Leu Ser Ile Tyr Leu
1370 1375 1380 1385

atg aaa tgt tca ccc atc ttg tat ata aaa tta tat gac agg ttt caa 4947
Met Lys Cys Ser Pro Ile Leu Tyr Ile Lys Leu Tyr Asp Arg Phe Gln
1390 1395 1400

aaa cag taagtaatca aaaattaaat taactcaatt accttttaaa ttataggagt 5003
Lys Gln

tgaaa atg aat tat agt atc att atg tcg gta tat aat gag cct tta aat 5053
Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn
1405 1410 1415

tat gtg aga gat tca gta gaa tct ata tta aat caa acg ctt act gat 5101
Tyr Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp

1420	1425	1430	
ttt gag ttc ata att gtc att gat aat cca agt aga ggt gat tta aag 5149			
Phe Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys			
1435	1440	1445	1450
caa ttc tta aca gaa tat tca gtt gta gat aat aga ata aaa atc ttg 5197			
Gln Phe Leu Thr Glu Tyr Ser Val Val Asp Asn Arg Ile Lys Ile Leu			
1455	1460	1465	
ctt aat gaa gaa aat att ggt tta gca tca agt ttg aac aaa gcg gtg 5245			
Leu Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val			
1470	1475	1480	
aaa att tct aag gga gaa tat att ttt aga atg gat gct gat gat att 5293			
Lys Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile			
1485	1490	1495	
tca tat cca agt aga ttt gat aag caa att cgt ttt atg gag gaa aat 5341			
Ser Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn			
1500	1505	1510	
tca ttg gat ttc tca gca act cta ata gaa ttg ata gac caa aaa gga 5389			
Ser Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly			
1515	1520	1525	1530
aat tta gta tat aaa caa cga gaa agt aat aaa ata tac tta act aat 5437			
Asn Leu Val Tyr Lys Gln Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn			
1535	1540	1545	
gat ata cgg aag atg tta ttg aat aga tct ata ctt gcc cac cca acg 5485			
Asp Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr			
1550	1555	1560	
tgg tgc gta aaa aag aaa gtt ttc gat aag tta atg gga tat aga gat 5533			
Trp Cys Val Lys Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp			
1565	1570	1575	
tta gta cct gtt gaa gat tat gat ttt gca ata aga gga gct ctg gct 5581			
Leu Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala			
1580	1585	1590	
gat ttc aaa atc ggc tta ctc aat aaa gta ctt tta cag tat aga tta 5629			
Asp Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu			
1595	1600	1605	1610

aac gag aat gga ata tca caa acc aat aag ttt aag caa tat att tac 5677
Asn Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr
1615 1620 1625

tca gct att tta caa gat ttt tat aaa gaa aaa tct tat att gat atc 5725
Ser Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile
1630 1635 1640

aca aaa att act aat tac ttt caa gag tat gtg ata aag aaa cgc tat 5773
Thr Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr
1645 1650 1655

act cag caa gag ctc tct aaa tat ttt gag cta aaa tct acc cct agt 5821
Thr Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser
1660 1665 1670

att act att aga aaa cta tat att tgt tta tat tta tac ttt aag tct 5869
Ile Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser
1675 1680 1685 1690

ccc ttg gtt agg agg tta tta ata aat gat att aat att tta gta ctg 5917
Pro Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu
1695 1700 1705

aaa ttg ttt gga gga gag aaa caa agt gac taatagaaaa atttatgtat 5967
Lys Leu Phe Gly Gly Glu Lys Gln Ser Asp
1710 1715

gtcactactct ttatcattta ttgatttggt tatataaaga agagatatat tcaaatttag 6027

aaattattct ctcttcttct attcctgatg ttgataattt agagaaaaaa ttaaaatcaa 6087

aaacaataaa tatacatatt ttagaagaat ctagtgggtga aagtgaagaa ttattatcag 6147

tacttaaaga tgctggtcta agttatagta agtttgatag taattgtttt attttaatg 6207

atgcaacgcc tattgggagg acactaataa agcatgggtat ttattataat ctaattgaag 6267

atggtttaaa ttgttttact tactctatat ttagtcaaaa actttggaag tattatgtaa 6327

aaaaatatat tcttcacaaa attcagccac atggattttc acgatattgt ttagggattg 6387

aagttaattc attagttaat ttgccaaagg atccgcgtta taaaaaattt attgaagtcc 6447

ctaggaaaga actttttgac aatgtaacag aatatcaaaa agaaatggca ataaatcttt 6507

ttggagcagt aagagttagt attaatcac cttcagtact agtattaacg cagcctctat 6567
 ctatagataa agagtttatg agttataaca ataagataga aacgtccgaa gaacaattta 6627
 atttttataa atcaatagtc aatgaatata taaataaagg gtacaatgtt tattttaaaag 6687
 ttcatcctag agatgtagta gattattcca aattgccggt agagctatta ccatcaaag 6747
 ttctatgga aattatagag ttgatgttaa caggtcggtt cgaatgtggg ataacacatt 6807
 cgtccactgc gctggatttt ttaactgtg ttgataaaaa aataacttta gtagatct 6865

<210> 4
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic DNA
 <400> 4
 gggggatcca atggattga aatacag

27

<210> 5
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic DNA
 <400> 5
 aatctgcaga ctagctcct gtcccagat

29

<210> 6
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic DNA
 <400> 6
 ccaagcggcc gctatagtca acttaaaagg tgg

33

<210> 7

<211> 28
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic DNA
<400> 7
cggctcgagt cccaataggc gttgcatc

28

<210> 8
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic DNA
<400> 8
ccggaattcg aaaaggtaaa gtgtctccga aa

32